IN THE CLAIM

Please amend claim 1 and add claims 25 through 30 to read as follows.

1. (Currently Amended) A process for quantitating a human DNA in a sample, said process comprising the steps of:

providing a sample to be analyzed;

amplifying predetermined genomic DNA of an *Alu* element subfamily by using primers, said *Alu* element subfamily being more enriched in the human genome than in any non-human primate ~~genom~~ genome, the amplification being intra-*Alu* polymerase chain reaction amplification; and

measuring the amount of the human DNA by comparing the amplified DNA with a reference to quantitate the human DNA in the sample.

2. (Canceled)

3. (Canceled)

4. (Canceled)

5. (Previously Presented) The process of claim 1, wherein the amplification is a polymerase chain reaction with the primers containing the following sequences:

5' CGAGGCGGGTGGATCATGAGGT 3'(SEQ ID NO: 3)

and

5' TCTGTCGCCCAGGCCGGACT 3' (SEQ ID NO: 4).

6. (Previously Presented) The process of claim 1, wherein the amplification is a polymerase chain reaction with the primers containing the following sequences:

5' GAGATCGAGACCACGGTGAAA 3' (SEQ ID NO: 5)

and

5' TTTGAGACGGAGTCTCGTT 3' (SEQ ID NO: 6).

7. (Previously Presented) The process of claim 1, wherein the measurement step comprises the step of measuring the amount of the human DNA on an agarose gel stained with ethidium bromide.

8. (Previously Presented) The process of claim 1, wherein the measurement step comprises the step of measuring the amount of the human DNA by using a qPCR system.

9. (Previously Presented) The process of claim 1, wherein the measurement step comprises the step of measuring the amount of the human DNA by using *Taq*Man chemistry.

Claims 10-20. (Canceled)

21. (Previously Presented) A process for quantitating a human DNA in a sample, said process comprising the steps of:

providing a sample to be analyzed;

amplifying predetermined genomic DNA containing an *Alu* element by using primers, said *Alu* element being present only in the human genome, the amplification being intra-*Alu* polymerase chain reaction amplification; and

measuring the amount of the human DNA by comparing the amplified DNA with a reference.

22. (Previously Presented) A process for quantitating a human DNA in a sample, said process comprising the steps of:

providing a sample to be analyzed;

amplifying predetermined genomic DNA of an *Alu* element subfamily by using primers, said predetermined genomic DNA including subfamily-specific diagnostic mutations, a copy number of said predetermined genomic DNA in the human genome being higher than a copy number of said predetermined genomic DNA in any non-human primate genome, the amplification being intra-*Alu* polymerase chain reaction amplification; and

measuring the amount of the human DNA by comparing the amplified DNA with a reference.

23. (Previously Presented) The process of claim 1, wherein each of said primers includes a subfamily-specific diagnostic mutation.

24. (Previously Presented) The process of claim 21, wherein each of said primers includes a subfamily-specific diagnostic mutation.

25. (New) The process of claim 1, wherein said Alu element subfamily is Yb8 subfamily.

26. (New) The process of claim 1, wherein said Alu element subfamily is Ya5 subfamily.

27. (New) The process of claim 1, wherein said Alu element subfamily is Yd6 subfamily.

28. (New) The process of claim 22, wherein said Alu element subfamily is Yb8 subfamily.

29. (New) The process of claim 22, wherein said Alu element subfamily is Ya5 subfamily.

30. (New) The process of claim 22, wherein said Alu element subfamily is Yd6 subfamily.